



OIPe

RAW SEQUENCE LISTING

DATE: 09/26/2003

PATENT APPLICATION: US/10/663,896

TIME: 09:45:00

Input Set : N:\Crif3\RULE60\US10663896.raw.txt

Output Set: N:\CRF4\09262003\J663896.raw

ENTERED

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1 <110> APPLICANT: Reinhard, Christoph
2 <120> TITLE OF INVENTION: HUMAN CYCLIN-DEPENDANT KINASE (hPNQALRE)
3 <130> FILE REFERENCE: 200130.459 / 1524.002
4 <140> CURRENT APPLICATION NUMBER: US/10/663,896
5 <141> CURRENT FILING DATE: 2003-09-16
6 <150> PRIOR APPLICATION NUMBER: US/09/464,065
7 <151> PRIOR FILING DATE: 1999-12-15
8 <160> NUMBER OF SEQ ID NOS: 17
9 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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11 <211> LENGTH: 1002
12 <212> TYPE: DNA
13 <213> ORGANISM: Homo sapien
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16      atcgtcttca aggccaagca cgtggagact ggcgagatag ttgccctcaa gaaggtggcc      120
17      ctaaggcggg tggaagacgg cttccctaac caggccctgc gggagattaa ggctctgcag      180
18      gagatggagg acaatcagta tgtggtacaa ctgaaggctg tgttcccaca cgggtggaggc      240
19      tttgtgctgg cctttgagtt catgctgtcg gatctggccg aggtggtgcy ccatgcccag      300
20      aggccactag cccaggcaca ggtcaagagc tacctgcaqa tgctgctcaa ggggtgctgcc      360
21      ttctgccatg ccaacaacat tgtacatcgg gacctgaaac ctgccaaacct gctcatcagc      420
22      gcctcaggcc agctcaagat agcggacttt ggcctggctc gactcttttc ccagacggc      480
23      agccgcctct acacacacca ggtggccacc aggtctgtgg gctgcatcat gggggagctg      540
24      ttgaatgggt cccccccttt cccgggcaag aacgatattg aacagctttg ctatgtgctt      600
25      cgcactcttg gcaccccaaa ccctcaagtc tggccggagc tcaactgagct gccggactac      660
26      aacaagatct cccttaagga gcagggtgcc atgccctgg aggaggtgct gcctgacgtc      720
27      tctccccagg cattggatct gctgggtcaa ttcttctct accctctca ccagcgcac      780
28      gcagcttcca aggtctcct ccatcagtag ttcttcacag ctcccctgcc tgcccatcca      840
29      tctgagctgc cgattcctca gcgtctaggg ggacctgccc ccaaggccca tccagggccc      900
30      cccacatcc atgacttcca cgtggaccgg cctcttgagg agtcgctggt gaacccagag      960
31      ctgattcggc ccttcacact ggagaggtga ggatcctgag aa      1002
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33 <211> LENGTH: 325
34 <212> TYPE: PRT
35 <213> ORGANISM: Homo sapien
36 <400> SEQUENCE: 2
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38      1          5          10          15
39      Ile Val Phe Lys Ala Lys His Val Glu Thr Gly Glu Ile Val Ala Leu
40      20          25          30
41      Lys Lys Val Ala Leu Arg Arg Leu Glu Asp Gly Phe Pro Asn Gln Ala
42      35          40          45
43      Leu Arg Glu Ile Lys Ala Leu Gln Glu Met Glu Asp Asn Gln Tyr Val

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48          50          55          60
49 Val Gln Leu Lys Ala Val Phe Pro His Gly Gly Gly Phe Val Leu Ala
50 65          70          75          80
51 Phe Glu Phe Met Leu Ser Asp Leu Ala Glu Val Val Arg His Ala Gln
52          85          90          95
53 Arg Pro Leu Ala Gln Ala Gln Val Lys Ser Tyr Leu Gln Met Leu Leu
54          100          105          110
55 Lys Gly Val Ala Phe Cys His Ala Asn Asn Ile Val His Arg Asp Leu
56          115          120          125
57 Lys Pro Ala Asn Leu Leu Ile Ser Ala Ser Gly Gln Leu Lys Ile Ala
58          130          135          140
59 Asp Phe Gly Leu Ala Arg Val Phe Ser Pro Asp Gly Ser Arg Leu Tyr
60          145          150          155          160
61 Thr His Gln Val Ala Thr Arg Ser Val Gly Cys Ile Met Gly Glu Leu
62          165          170          175
63 Leu Asn Gly Ser Pro Leu Phe Pro Gly Lys Asn Asp Ile Glu Gln Leu
64          180          185          190
65 Cys Tyr Val Leu Arg Ile Leu Gly Thr Pro Asn Pro Gln Val Trp Pro
66          195          200          205
67 Glu Leu Thr Glu Leu Pro Asp Tyr Asn Lys Ile Ser Leu Lys Glu Gln
68          210          215          220
69 Val Pro Met Pro Leu Glu Glu Val Leu Pro Asp Val Ser Pro Gln Ala
70          225          230          235          240
71 Leu Asp Leu Leu Gly Gln Phe Leu Leu Tyr Pro Pro His Gln Arg Ile
72          245          250          255
73 Ala Ala Ser Lys Ala Leu Leu His Gln Tyr Phe Phe Thr Ala Pro Leu
74          260          265          270
75 Pro Ala His Pro Ser Glu Leu Pro Ile Pro Gln Arg Leu Gly Gly Pro
76          275          280          285
77 Ala Pro Lys Ala His Pro Gly Pro Pro His Ile His Asp Phe His Val
78          290          295          300
79 Asp Arg Pro Leu Glu Glu Ser Leu Leu Asn Pro Glu Leu Ile Arg Pro
80          305          310          315          320
81 Phe Ile Leu Glu Arg
82          325
84 <210> SEQ ID NO: 3
85 <211> LENGTH: 1053
86 <212> TYPE: DNA
87 <213> ORGANISM: Homo sapien
88 <400> SEQUENCE: 3
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90 gccaaagcacg tggagactgg cgagatagtt gccctcaaga aggtggccct aaggcggttg 120
91 gaagacggct tccctaacca ggccctgcgg gagattaagg ctctgcagga gatggaggac 180
92 aatcagtatg tggtaacaact gaaggctgtg ttccacacag gtggaggctt tgtgctggcc 240
93 tttgagttca tgctgtcgga tctggccgag gtggtgcgcc atgccagag gccgctagcc 300
94 caggcacagg tcaagagcta cctgcagatg ctgctcaagg gtgtgcctt ctgccatgcc 360
95 aacaacattg tacatcggga cctgaaacct gccaacctgc tcatcagcgc ctcaggccag 420
96 ctcaagatag cggactttgg cctggctcga gtcttttccc cagacggcag ccgcctctac 480
97 acacaccagg tggccaccag gtggtaccga gcccccgagc tctgttatgg tgcccgccag 540

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98      tatgaccagg gcgtcgatct gtgggtctgtg ggctgcatca tgggggagct gttgaatggg      600
99      tcccccccttt tcccgggcaa gaacgatatt gaacagcttt gctatgtgct tcgcatcttg      660
100     ggcaccccaa accctcaagt ctggcccgag ctactgagc tgccggacta caacaagatc      720
101     tcctttaagg agcaggtgcc catgcccctg gaggaggtgc tgcctgacgt ctctccccag      780
102     gcattggatc tgcctgggtca attccttctc taccctcctc accagcgcat cgcagcttcc      840
103     aaggctctcc tccatcagta cttcttcaca gctcccctgc ctgcccaccc atctgagctg      900
104     ccgattcctc agcgtctagg gggacctgcc cccaaggccc atccagggcc cccccacatc      960
105     catgacttcc acgtggaccg gcctcttgag gagtcgctgt tgaaccacga gctgattcgg      1020
106     cccttcaccc tggaggggtg aggatcctga gaa                                1053
108 <210> SEQ ID NO: 4
109 <211> LENGTH: 346
110 <212> TYPE: PRT
111 <213> ORGANISM: Homo sapien
112 <400> SEQUENCE: 4
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114         1             5             10             15
115     Ile Val Phe Lys Ala Lys His Val Glu Thr Gly Glu Ile Val Ala Leu
116             20             25             30
117     Lys Lys Val Ala Leu Arg Arg Leu Glu Asp Gly Phe Pro Asn Gln Ala
118             35             40             45
119     Leu Arg Glu Ile Lys Ala Leu Gln Glu Met Glu Asp Asn Gln Tyr Val
120             50             55             60
121     Val Gln Leu Lys Ala Val Phe Pro His Gly Gly Phe Val Leu Ala
122             65             70             75             80
123     Phe Glu Phe Met Leu Ser Asp Leu Ala Glu Val Val Arg His Ala Gln
124             85             90             95
125     Arg Pro Leu Ala Gln Ala Gln Val Lys Ser Tyr Leu Gln Met Leu Leu
126             100            105            110
127     Lys Gly Val Ala Phe Cys His Ala Asn Asn Ile Val His Arg Asp Leu
128             115            120            125
129     Lys Pro Ala Asn Leu Leu Ile Ser Ala Ser Gly Gln Leu Lys Ile Ala
130             130            135            140
131     Asp Phe Gly Leu Ala Arg Val Phe Ser Pro Asp Gly Ser Arg Leu Tyr
132             145            150            155            160
133     Thr His Gln Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu Tyr
134             165            170            175
135     Gly Ala Arg Gln Tyr Asp Gln Gly Val Asp Leu Trp Ser Val Gly Cys
136             180            185            190
137     Ile Met Gly Glu Leu Leu Asn Gly Ser Pro Leu Phe Pro Gly Lys Asn
138             195            200            205
139     Asp Ile Glu Gln Leu Cys Tyr Val Leu Arg Ile Leu Gly Thr Pro Asn
140             210            215            220
141     Pro Gln Val Trp Pro Glu Leu Thr Glu Leu Pro Asp Tyr Asn Lys Ile
142             225            230            235            240
143     Ser Phe Lys Glu Gln Val Pro Met Pro Leu Glu Glu Val Leu Pro Asp
144             245            250            255
145     Val Ser Pro Gln Ala Leu Asp Leu Leu Gly Gln Phe Leu Leu Tyr Pro
146             260            265            270
147     Pro His Gln Arg Ile Ala Ala Ser Lys Ala Leu Leu His Gln Tyr Phe

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148          275          280          285
149 Phe Thr Ala Pro Leu Pro Ala His Pro Ser Glu Leu Pro Ile Pro Gln
150          290          295          300
151 Arg Leu Gly Gly Pro Ala Pro Lys Ala His Pro Gly Pro Pro His Ile
152 305          310          315          320
153 His Asp Phe His Val Asp Arg Pro Leu Glu Glu Ser Leu Leu Asn Pro
154          325          330          335
155 Glu Leu Ile Arg Pro Phe Ile Leu Glu Arg
156          340          345
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159 <211> LENGTH: 1092
160 <212> TYPE: DNA
161 <213> ORGANISM: Homo sapien
162 <400> SEQUENCE: 5
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164 gccaagcacg tggagccgag ggtgggctgg cagtgtctgc cttctatcct gcagactggc      120
165 gagatagttg ccctcaagaa ggtggcccta aggcggttgg aagacggctt ccctaaccag      180
166 gccctgcggg agattaaggc tctgcaggag atggaggaca atcagtatgt ggtacaactg      240
167 aaggctgtgt tcccacacgg tggaggcttt gtgctggcct ttgagttcat gctgtcggat      300
168 ctggccgagg tgggtgcgcca tgcccagagg ccactagccc aggcacaggc caagagctac      360
169 ctgcagatgc tgctcaaggg tgctgccttc tgccatgcca acaacattgt acatcgggac      420
170 ctgaaacctg ccaacctgct catcagcgcc tcaggccagc tcaagatagc ggactttggc      480
171 ctggctcgag tcttttcccc agacggcagc cgctctaca cacaccaggc ggccaccagg      540
172 tggtagcgag ccccgagct cctgtatggc gcccggcagt atgaccaggc cgtcgatctg      600
173 tggctctgtg gctgcatcat gggggagctg ttgaatgggt cccccctttt cccgggcaag      660
174 aacgatattg aacagctttg ctatgtgctt cgcatcttgg gcacccccaa cctcaagtc      720
175 tggccggagc tcactgagct gccggactac aacaagatct cctttaagga gcagggtgcc      780
176 atgcccctgg aggaggtgct gcctgacgtc tctccccagg cattggatct gctgggtcaa      840
177 ttccttctct accctcctca ccagcgcata gcagcttcca aggtctcct ccatcagtag      900
178 ttcttcacag ctcccctgcc tgcccatcca tctgagctgc cgtttcctca gcgtctaggg      960
179 ggacctgccc ccaaggccca tccagggcc cccacatcc atgacttcca cgtggaccgg      1020
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181 ggatcctgag aa                                     1092
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184 <211> LENGTH: 359
185 <212> TYPE: PRT
186 <213> ORGANISM: Homo sapien
187 <400> SEQUENCE: 6
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190 Ile Val Phe Lys Ala Lys His Val Glu Pro Arg Val Gly Trp Gln Cys
191          20          25          30
192 Leu Pro Ser Ile Leu Gln Thr Gly Glu Ile Val Ala Leu Lys Lys Val
193          35          40          45
194 Ala Leu Arg Arg Leu Glu Asp Gly Phe Pro Asn Gln Ala Leu Arg Glu
195          50          55          60
196 Ile Lys Ala Leu Gln Glu Met Glu Asp Asn Gln Tyr Val Val Gln Leu
197          65          70          75          80
198 Lys Ala Val Phe Pro His Gly Gly Gly Phe Val Leu Ala Phe Glu Phe

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199          85          90          95
200 Met Leu Ser Asp Leu Ala Glu Val Val Arg His Ala Gln Arg Pro Leu
201          100          105          110
202 Ala Gln Ala Gln Val Lys Ser Tyr Leu Gln Met Leu Leu Lys Gly Val
203          115          120          125
204 Ala Phe Cys His Ala Asn Asn Ile Val His Arg Asp Leu Lys Pro Ala
205          130          135          140
206 Asn Leu Leu Ile Ser Ala Ser Gly Gln Leu Lys Ile Ala Asp Phe Gly
207          145          150          155          160
208 Leu Ala Arg Val Phe Ser Pro Asp Gly Ser Arg Leu Tyr Thr His Gln
209          165          170          175
210 Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu Tyr Gly Ala Arg
211          180          185          190
212 Gln Tyr Asp Gln Gly Val Asp Leu Trp Ser Val Gly Cys Ile Met Gly
213          195          200          205
214 Glu Leu Leu Asn Gly Ser Pro Leu Phe Pro Gly Lys Asn Asp Ile Glu
215          210          215          220
216 Gln Leu Cys Tyr Val Leu Arg Ile Leu Gly Thr Pro Asn Pro Gln Val
217          225          230          235          240
218 Trp Pro Glu Leu Thr Glu Leu Pro Asp Tyr Asn Lys Ile Ser Phe Lys
219          245          250          255
220 Glu Gln Val Pro Met Pro Leu Glu Glu Val Leu Pro Asp Val Ser Pro
221          260          265          270
222 Gln Ala Leu Asp Leu Leu Gly Gln Phe Leu Leu Tyr Pro Pro His Gln
223          275          280          285
224 Arg Ile Ala Ala Ser Lys Ala Leu Leu His Gln Tyr Phe Phe Thr Ala
225          290          295          300
226 Pro Leu Pro Ala His Pro Ser Glu Leu Pro Val Pro Gln Arg Leu Gly
227          305          310          315          320
228 Gly Pro Ala Pro Lys Ala His Pro Gly Pro Pro His Ile His Asp Phe
229          325          330          335
230 His Val Asp Arg Pro Leu Glu Glu Ser Leu Leu Asn Pro Glu Leu Ile
231          340          345          350
232 Arg Pro Phe Ile Leu Glu Gly
233          355
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236 <211> LENGTH: 1038
237 <212> TYPE: DNA
238 <213> ORGANISM: Homo sapien
239 <400> SEQUENCE: 7
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242 gagatagttg ccctcaagaa ggtggcccta aggcggttgg aggaaggctt cctaaccag      180
243 gccctgcggg agattaaggc tctgcaggag atggaggaca atcagtatgt ggtacaactg      240
244 aaggctgtgt tcccacacgg tggaggcttt gtgctggcct ttgagttcat gctgtcggat      300
245 ctggccgagg tgggtgcgcca tgcccagagg ccactagccc aggcacaggt caagagctac      360
246 ctgcagatgc tgctcaaggg tgtcgccttc tgccatgcc acaacattgt acatcgggac      420
247 ctgaaacctg ccaacctgct catcagcgcc tcaggccagc tcaagatagc ggactttggc      480
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